

INVESTIGATION OF THE VALIDITY OF HIGHLY EVOLVED ASTEROID FAMILIES. M. S. Kelley and M. J. Gaffey, Department of Earth & Environmental Science, West Hall G-17, Rensselaer Polytechnic Institute, Troy, NY 12180-3590, kellem@rpi.edu, gaffem@rpi.edu.

The extent of collisional evolution of the asteroid population and the total mass loss from this region of the solar system are fundamental questions related to the origin of the solar system. Of particular interest is whether or not the region of the asteroid belt represented a local minimum in the heliocentric mass distribution in the late solar nebula and/or the very early solar system. Theoretical models of collisional evolution for both high mass and low mass asteroidal regions can produce the presently observed asteroid size frequency distribution [e.g. 1,2]. Unfortunately, these investigations cannot distinguish between the case where a significant mass loss has occurred in the asteroidal region and the case where this was initially a low mass region.

One approach to discriminating between the high mass (large mass loss) and the low mass (small mass loss) cases utilizes asteroid families. A true or genetic asteroid family is formed by a large impact onto or a collision with a parent object. At one end of the sequence are families formed by large cratering events in which the parent body is left essentially intact while supplying a retinue of smaller objects [3]. The Vesta family is commonly cited as an example of such a "cratering event family". At the other end of the sequence are families formed by the collisional breakup of the parent body, resulting in a range of sizes extending down from the largest fragment, which is substantially smaller than the original parent body. The Koronis, Eos, and Themis families are commonly cited as examples of such "parent body disruption" families. In the case of a family generated by the disruption of a completely differentiated parent body, it is reasonable to assume that, given enough time, the family may be reduced to only a few relatively large and/or strong (metal-rich) members. Disruption of a homogeneous parent body might be expected to yield a more uniform size distribution over time.

Since an asteroid family starts with a small (compared to the asteroid belt as a whole) mass and membership, it will evolve in a specific direction because the smaller and weaker (silicate-rich) family members have collisional lifetimes much shorter than the age of the solar system. The smaller family members can only be replenished by breakup of a larger family member. Since the lifetime against collisional disruption increases with size and strength, the smaller and weaker family members will tend to disappear leaving only a few larger or stronger bodies [4]. After the family reaches maturity, only intermittently will the smaller family members be replenished by the relatively rare collisional disruption of one of the large family objects. These highly evolved families will become increasingly dominated by the larger and/or stronger members. For example, a family formed by the collisional disruption of a fully differentiated parent body will include metallic core fragments and silicate mantle and crustal fragments, with an

initial metal/silicate ratio which depends on the chondritic chemical group of the parent body. Due to the different strengths of metal- and silicate-rich objects, the metal/silicate ratio in the family will increase with time and thus provide a measure of relative family age.

If the existence of such highly evolved asteroid families can be confirmed, it would indicate that collisional evolution had proceeded sufficiently to remove large portions of the initial families. This would provide strong evidence in favor of the high mass loss model and a massive original asteroid belt since the general asteroid population should have experienced a similar degree of collisional evolution and mass depletion. If highly evolved asteroid families are absent from the asteroid belt, it would indicate comparably little mass loss for the general asteroid population. It also would support a low mass original asteroid belt and a mass minimum in the solar nebula or the very early solar system in the asteroidal region.

Williams [5,6] has identified a number of dynamical families which include only a few members each. Although there is considerable debate over the validity of these small families, they fit the profile for highly evolved families. We are investigating a subset of the small Williams families to test whether they are genetic families. If the genetic validity of a number of these families can be confirmed, it would provide strong evidence for the high mass case. If few or none can be confirmed, it would indicate that either the small Williams families are invalid or that the initial low mass model for the asteroidal region is probably correct.

Following Hirayama's original discovery of and subsequent work on asteroid families [7,8], many dynamical studies of asteroid families were done [5,9-12]. Chapman *et al.* [13] raised the question "...are the family groupings identified by various researchers composed of 'true', genetically related asteroids - are the families 'real'?" This is still a critical issue in the area of asteroid family studies. While this decade has seen several additional dynamical studies of asteroid families [e.g. 6,14-16], it is still unclear which of the various methods, if any, accurately identifies asteroid family memberships.

In the quest for identification of genetic (a.k.a. "true" or "real") asteroid families within the various dynamical family classifications, several taxonomic studies were undertaken [e.g. 17- 19]. Unfortunately, even the most recent taxonomic study, using 0.44-0.92 μ m (visible region) spectral reflectance data [20], falls short of demonstrating true genetic relationships. In the isolated case of the Vesta family [21], the fortuitously unique visible to near-IR spectrum of 4 Vesta allowed spectral matching with members that had less complete wavelength coverage.

The aforementioned studies have shown that dynamical and taxonomic studies of asteroid families typically only point out possible family memberships or interlopers. They

were unable to identify probable or even plausible relationships between asteroids. Only direct sampling and petrologic analysis of asteroids has any chance of absolutely defining genetic relationships. However, a detailed compositional study, combining ground-based, visible and near-IR (approx. 0.4-2.6 μ m) spectral data, of dynamically associated asteroids can show where probable genetic relationships exist.

From collisional and geological evolution perspectives, an accurate method for determining asteroid family membership must allow for highly evolved families. To date the only dynamical asteroid family classification scheme to consistently identify very small, and presumably relatively old families, is that of Williams [5,6]. The Metis family (Williams #170), including 9 Metis and 113 Amalthea, provides a good example of what might be the evolutionary end of a family. Based on current diameter estimates for these 2 objects [22], as much as 86% of their original parent body has been lost. While both of these asteroids may fall within the same family in a different classification [e.g. 12], no other scheme identifies this group as a separate family. A previous, preliminary evaluation of this pair [23] based on existing 52- and 24-color survey data indicated they were a plausible genetic family. Analyses of recent, more continuous spectral data indicate there is a probable genetic link between these two asteroids. This does not imply that classification systems other than Williams' [5,6] are incorrect or that their methods are invalid. Instead, the present study and previous work [23,24] show that there is a growing number of compositional signatures for small, genetic asteroid families. Dynamical family classification schemes which identify fewer, but larger families that include these smaller, compositionally distinct (genetic) families may now be evaluated to see if their members match the genetic subsets.

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